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Ford, Vanessa

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Phone: 703.308.4735

FB DISCLOSURE, FIG 13B,

XX The invention provides isolated outer membrane proteins (OMP) from
 CC Ehrlichia chaffeensis and E. canis. The E. chaffeensis proteins form part
 CC of the OMP family and consist of proteins OMP-1, -1(B to Z) shown
 CC in AAY06943-958. The E. canis proteins form part of the P30 family and
 CC consist of proteins shown in AAY06959-970. The proteins and genes are
 CC used to detect E. chaffeensis in patients and E. canis in dogs.
 XX
 SQ Sequence. 288 AA;

Query Match 100.0%; Score 110; DB 20; Length 288;
 Best Local Similarity 100.0%; Pred. No. 1.5e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTTTGVFLKQDWGATIKD 20
 |||||
 Db 60 ntttgvgfklqgdwgatikd 79

RESULT 2

AAV06948
 ID AAY06948 standard; Protein; 280 AA.

XX AC AAY05948;

XX DT 05-JUL-1999 (first entry)

XX DE E. chaffeensis OMP-1F protein.

XX KW Outer membrane protein; OMP; Ehrlichia chaffeensis; E. canis; P30;
 XX detection; dog.

XX OS Ehrlichia chaffeensis.

XX PN WO9913720-A1.

XX PD 25-MAR-1999.

XX PF 18-SEP-1998; 98WO-US19600.

XX PR 19-SEP-1997; 97US-0059353.

XX PA (OHIS) UNIV OHIO STATE.

XX PI Ohashi N, Rikihisa Y;

XX PR WPI; 1999-254290/21.

XX DR N-PSDB; AAX34748.

XX PT Novel outer membrane proteins from Ehrlichia chaffeensis and
 XX Ehrlichia canis

XX PS Claim 16; Fig 8B; 55pp; English.

XX The invention provides isolated outer membrane proteins (OMP) from
 CC Ehrlichia chaffeensis and E. canis. The E. chaffeensis proteins form part
 CC of the OMP family and consist of proteins OMP-1, -1(B to Z) shown
 CC in AAY06943-958. The E. canis proteins form part of the P30 family and
 CC consist of proteins shown in AAY06959-970. The proteins and genes are
 CC used to detect E. chaffeensis in patients and E. canis in dogs.
 XX

SQ Sequence 280 AA;

Query Match 87.3%; Score 96; DB 20; Length 280;
 Best Local Similarity 94.4%; Pred. No. 2.5e-07;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTTTGVFLKQDWGATII 18
 |||||
 Db 60 ntttgvgfklqgdwgatI 77

RESULT 3

AAW51094
 ID AAW51094 standard; Protein; 280 AA.

XX AC AAW51094;

XX DT 14-SEP-1998 (first entry)

XX DE Ehrlichia chaffeensis VSA4 protein.

XX KW MAP1 homologue; variable surface antigen; VSA4; rickettsia;
 XX DNA vaccine.

XX OS Ehrlichia chaffeensis.

XX FH Key Location/Qualifiers

XX FT Peptide 1..25

XX FT /note= "putative signal peptide"

XX PN WO9816554-A1.

XX PD 23-APR-1998.

XX PF 17-OCT-1997; 97WO-US19044.

XX PR 17-OCT-1996; 96US-0733230.

XX PA (UYEL) UNIV FLORIDA.

XX PI Barbet AF, Burridge MJ, Santa RR, Mahan SM, McGuire TC;

XX PI Nyika A, Rurangirwa FR;

XX DR WPI; 1998-251232/22.

XX DR N-PSDB; AAV071179.

XX Composition containing nucleic acid encoding rickettsial antigen -
 XX useful for, e.g. stimulating protective immune response in humans or
 XX animals

XX PS Claim 3; Fig 2B; 39pp; English.

XX This is the full-length variable surface antigen VSA4 protein of
 CC Ehrlichia chaffeensis. Its amino acid sequence was deduced from a
 CC partial open reading frame (ORF4) of a genomic locus (see AAV071179)
 CC of E. chaffeensis that was obtained on the basis of homology to the
 CC major antigenic protein MAP1 (see AAW51088) of Cowdria ruminantium.
 CC This genomic locus included 5 ORFs encoding similar, but
 CC non-identical proteins (see AAW51091-95). A claimed composition
 CC comprises a nucleic acid (see AAV07176-82) encoding a polypeptide
 CC (see AAW51088-99) that elicits a protective immune response against a
 CC rickettsial pathogen. The nucleic acid is used, in human or
 CC veterinary medicine, in vaccines to protect against Rickettsia,
 CC Ehrlichia, Anaplasma and Cowdria species. The Ehrlichia antigenic
 CC polypeptides can be used diagnostically to detect antibodies
 CC associated with Ehrlichia infection (claimed).
 XX

SQ Sequence 280 AA;

Query Match 81.8%; Score 90; DB 19; Length 280;
 Best Local Similarity 88.9%; Pred. No. 2.3e-06;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NTTTGVFLKQDWGATII 18
 |||||
 Db 60 ntttgvgfklqgdwgstI 77

RESULT 4

AAB36188
 ID AAB36188 standard; Protein; 280 AA.

XX

AC AAB36188;
 XX 02-MAR-2001 (first entry)
 DT Ehrlichia chaffeensis partial VSA4.
 DE
 XX
 DE Ehrlichia chaffeensis; VSA4; variable surface antigen 4; MAP1;
 KW major antigenic protein 1; antirickettsial; vaccine; gene therapy;
 KW Rickettsia; Cowdria; Anaplasma; map2; lhworf3; 4hworf1; 18hworf1;
 KW 3gdorf3.
 XX
 XX Ehrlichia chaffeensis.
 OS
 XX WO2000065063-A2.
 PN
 XX
 XX 02-NOV-2000.
 PD
 XX
 XX 21-APR-2000; 2000WO-US10886.
 PF
 XX 22-APR-1999; 99US-0130725.
 PR
 XX (UYFL) UNIV FLORIDA.
 PA
 XX Barbet AF, Bowie MV, Ganta RR, Burridge MJ, Mahan SM, McGuire TC;
 PI Rurangirwa FR, Moreland AL, Simbi BH, Whitnair WW, Allenan AR;
 PI WPI; 2000-679675/66.
 DR N-PSDB; AAC68705.
 DR
 XX New polynucleotides useful as DNA vaccines for conferring immunity to
 PT rickettsial infection e.g. heartwater caused by Cowdria ruminantium,
 PT comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
 PT
 XX Claim 3; Page 45-46; 63pp; English.
 PS
 XX The present sequence shows a high degree of similarity to the major
 CC antigenic protein 1 (MAP1) of Ehrlichia sp. The MAP1 gene may be
 CC used in a vaccines to protect animals or humans against rickettsial
 CC diseases caused by a organisms of Rickettsia sp., Ehrlichia sp.,
 CC Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response
 CC protective against the rickettsial pathogen. The nucleic acid vaccines
 CC can be driven by the human cytomegalovirus (HCMV) enhancer-promoter.
 CC Cowdria ruminantium genes designated map 2, lhworf3, 4hworf1, 18hworf1
 CC and 3gdorf3 may be used in therapeutic and diagnostic applications. The
 CC polypeptides are useful for detecting antibodies associated with
 CC infection by a rickettsial pathogen whilst the polynucleotides may be
 CC used to detect the presence of rickettsial nucleic acids.
 XX
 XX Sequence 280 AA;
 SQ

Query Match 81.8%; Score 90; DB 21; Length 280;
 Best Local Similarity 88.9%; Pred. No. 2.3e-06;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NTGTGVLKQDWGATI 18
 ||| |||||
 DB 60 ntgtgvlkqdwgstl 77

RESULT 5
 AAU04198
 ID AAU04198 standard; Protein; 280 AA.
 XX
 AC AAU04198;
 XX
 DT 23-OCT-2001 (first entry)
 XX
 DE Variable surface antigen 4 (VSA4) from Ehrlichia chaffeensis.
 XX
 KW Major antigenic protein; MAP; vaccine; immunogenic; rickettsia;
 KW infection; heartwater; diagnostic; variable surface antigen; VSA.

XX Ehrlichia chaffeensis.
 OS
 XX US6251872-B1.
 PN
 XX 26-JUN-2001.
 PD
 XX 17-OCT-1997; 97US-0953326.
 PF
 XX 17-OCT-1996; 96US-0733230.
 PR
 XX (UYFL) UNIV FLORIDA.
 PA
 XX Barbet AF, Ganta RR, McGuire TC, Burridge MJ, Nyika A;
 PI Rurangirwa FR, Mahan SM, Bowie MV, Allenan AR;
 PI WPI; 2001-424487/45.
 DR N-PSDB; AAS07578.
 DR
 XX New MAP2 genes and polypeptides useful as vaccines for conferring
 PT immunity to human and animal rickettsial diseases, e.g. heartwater, or
 PT as molecular markers in nucleic acid analysis procedures
 PT
 XX Example 3; Fig 2A-2B; 30pp; English.
 PS
 XX The sequence represents the amino acid sequence of variable surface
 CC antigen 4 (VSA4) isolated from Ehrlichia chaffeensis, which
 CC has similarity to major antigen protein (MAP). The MAP polynucleotides
 CC and polypeptides are useful as vaccines for conferring immunity to
 CC rickettsia infection, including Cowdria ruminantium causing heartwater.
 CC The MAP polynucleotides may be used as molecular markers in nucleic acid
 CC analysis procedures, and to produce the MAP polypeptides, which may
 CC be used to raise antibodies that are reactive with the polypeptides.
 CC The nucleic acids may further be used as probes to identify
 CC complementary sequences within other nucleic acid molecules or genomes,
 CC where such probes can be applied to identify or distinguish infectious
 CC strains of organisms in diagnostic procedures or in rickettsial
 CC research where identification of particular organisms or strains is
 CC needed.
 XX
 XX Sequence 280 AA;
 SQ

Query Match 81.8%; Score 90; DB 22; Length 280;
 Best Local Similarity 88.9%; Pred. No. 2.3e-06;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NTGTGVLKQDWGATI 18
 ||| |||||
 DB 60 ntgtgvlkqdwgstl 77

RESULT 6
 AAU06942
 ID AAU06942 standard; Protein; 256 AA.
 XX
 AC AAU06942;
 XX
 DT 05-JUL-1999 (first entry)
 DT
 XX E. chaffeensis p28 protein.
 DE
 XX Outer membrane protein; OMP; Ehrlichia chaffeensis; E. canis; P30;
 KW detection; dog.
 KW
 XX Ehrlichia chaffeensis.
 OS
 XX WO9913720-A1.
 PN
 XX 25-MAR-1999.
 PD
 XX 18-SEP-1998; 98WO-US19600.
 PF
 XX

PR 19-SEP-1997; 97US-0059353.

XX (OHIS) UNIV OHIO STATE.

XX Ohashi N, Rikihisa Y;

XX WPI; 1999-254290/21.

DR N-PSDB; AAX34742.

XX Novel outer membrane proteins from Ehrlichia chaffeensis and
XX Ehrlichia canis

XX Claim 18; Fig 1: 55pp; English.

XX The invention provides isolated outer membrane proteins (OMP) from
XX Ehrlichia chaffeensis and E. canis. The E. chaffeensis proteins form part
XX of the OMP family and consist of proteins OMP-1, -1(B to 2) shown
XX in AY06943-958. The E. canis proteins form part of the P30 family and
XX consist of proteins shown in AY06959-970. The proteins and genes are
XX used to detect E. chaffeensis in patients and E. canis in dogs.

XX Sequence 256 AA;

Query Match 74.5%; Score 82; DB 20; Length 256;

Best Local Similarity 70.0%; Pred. No. 4e-05;

Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 NTTGVFGLKODWDGATIKD 20

||| ||||| ||||| |||||

3% nttvgvfglkqndgsaisn.53

RESULT 7

AAW51095

ID AAW51095 standard; Protein; 276 AA.

XX AAW51095;

XX 14-SEP-1998 (first entry)

XX Ehrlichia chaffeensis VSA5 protein (partial sequence).

XX MAP1 homologue; variable surface antigen; VSA5; rickettsia;
XX DNA vaccine.

XX Ehrlichia chaffeensis.

XX Key Location/Qualifiers

XX Peptide 1..25

XX /note= "putative signal peptide"

XX W09816554-A1.

XX 23-APR-1998.

XX 17-OCT-1997; 97WO-US19044.

XX 17-OCT-1996; 96US-0733230.

XX (UVFL) UNIV FLORIDA.

XX Barbet AF, Burridge MJ, Ganta RR, Mahan SM, McGuire TC;

XX Nyika A, Rurangirwa FR;

XX WPI; 1998-251232/22.

XX DR N-PSDB; AAV07179.

XX Composition containing nucleic acid encoding rickettsial antigen -

XX useful for, e.g. stimulating protective immune response in humans or

XX animals

XX Claim 3; Fig 2B; 39pp; English.

XX

CC This is the near full-length variable surface antigen VSA5 protein
CC of Ehrlichia chaffeensis; it lacks about 5-7 C-terminal amino acid
CC residues. The VSA5 amino acid sequence was deduced from a partial
CC open reading frame (ORF5) of a genomic locus (see AAV07179) of E.
CC chaffeensis that was obtained on the basis of homology to the major
CC antigenic protein MAP1 (see AAW51088) of Cowdria ruminantium. This
CC genomic locus included 5 ORFs encoding similar, but non-identical
CC proteins (see AAW51091-95). A claimed composition comprises a
CC nucleic acid (see AAV07176-82) encoding a polypeptide (see AAW51088-99)
CC that elicits a protective immune response against a rickettsial
CC pathogen. The nucleic acid is used, in human or veterinary
CC medicine, in vaccines to protect against Rickettsia, Ehrlichia,
CC Anaplasma and Cowdria species. The Ehrlichia antigenic
CC polypeptides can be used diagnostically to detect antibodies
CC associated with Ehrlichia infection (claimed).

XX Sequence 276 AA;

Query Match 74.5%; Score 82; DB 19; Length 276;

Best Local Similarity 70.0%; Pred. No. 4.3e-05;

Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 NTTGVFGLKODWDGATIKD 20

||| ||||| ||||| |||||

59 nttvgvfglkqndgsaisn 78

RESULT 8

AA836189

ID AAB36189 standard; Protein; 276 AA.

XX AAB36189;

XX 02-MAR-2001 (first entry)

XX Ehrlichia chaffeensis partial VSA5.

XX Ehrlichia chaffeensis; VSA5; variable surface antigen 5; MAP1;

XX major antigenic protein 1; antirickettsial; vaccine; gene therapy;

XX Rickettsia; Cowdria; Anaplasma; map2; lhworf3; 4hworf1; 18hworf1;

XX 3gdorf3.

XX Ehrlichia chaffeensis.

XX WO200065063-A2.

XX 02-NOV-2000.

XX 21-APR-2000; 2000WO-US10886.

XX 22-APR-1999; 99US-0130725.

XX (UVFL) UNIV FLORIDA.

XX Barbet AF, Bowie MV, Ganta RR, Burridge MJ, Mahan SM, McGuire TC;

XX Rurangirwa FR, Moreland AL, Simbi BH, Whitmire WW, Alleman AR;

XX WPI; 2000-679675/66.

XX N-PSDB; AAC68706.

XX New polynucleotides useful as DNA vaccines for conferring immunity to
XX rickettsial infection e.g. heartwater caused by Cowdria ruminantium,
XX comprises major antigenic protein 1 or 2 gene of rickettsial pathogens

XX Claim 3; Page 47; 63pp; English.

XX The present sequence shows a high degree of similarity to the major
XX antigenic protein 1 (MAP1) of Ehrlichia sp. The MAP1 gene may be
XX used in a vaccine to protect animals or humans against rickettsial
XX diseases caused by a organisms of Rickettsia sp., Ehrlichia sp.,

XX

QY 1 NNTTGVFGLKQDWDGATIKD 20
 ||| |||||:|||:| :
 Db 60 nttvqvfglkanwdqasatn 79

RESULT 11
 AAB36183
 ID AAB36183 standard; Protein: 280 AA.
 XX
 AC AAB36183;
 DT 02-MAR-2001 (first entry)
 XX
 DE Ehrlichia chaffeensis MAP1.
 XX
 KW Ehrlichia chaffeensis; MAP1; major antigenic protein 1; antirickettsial;
 KW vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; lhworf3;
 KW 4hworfl; 18hworfl; 3gdorf3.
 XX
 OS Ehrlichia chaffeensis.
 XX
 PN W0200065063-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 21-APR-2000; 2000WO-US10886.
 XX
 PR 22-APR-1999; 99US-0130725.
 XX
 PA (UYEL) UNIV FLORIDA.
 XX
 PI Barbet AF, Bowie MV, Ganta RR, Burridge MJ, Mahan SM, McGuire TC;
 PI Rurangirwa FR, Moreland AL, Simbi BH, Whitmire WW, Alleman AR;
 XX
 DR WPI: 2000-679675/66.
 DR N-PSDB; AAC68700.
 XX
 PT New polynucleotides useful as DNA vaccines for conferring immunity to
 PT rickettsial infection e.g. heartwater caused by Cowdria ruminantium,
 PT comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
 PT
 XX
 PS Claim 3; Page 35-36; 63pp; English.
 XX
 CC The present sequence is given in a specification relating to nucleic
 CC acid vaccines containing genes to protect animals or humans against
 CC rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia
 CC sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response
 CC protective against the rickettsial pathogen. The vaccine comprises the
 CC major antigenic protein 1 (MAP1) gene or the major antigenic protein 2
 CC (MAP2) gene of rickettsial pathogens. The nucleic acid vaccines can be
 CC driven by the human cytomegalovirus (HCMV) enhancer-promoter. Cowdria
 CC ruminantium genes designated map 2, lhworf3, 4hworfl, 18hworfl and
 CC 3gdorf3 may be used in therapeutic and diagnostic applications. The
 CC polypeptides are useful for detecting antibodies associated with
 CC infection by a rickettsial pathogen whilst the polynucleotides may be
 CC used to detect the presence of rickettsial nucleic acids.
 XX
 SQ Sequence 280 AA;
 Query Match 74.5%; Score 82; DB 21; Length 280;
 Best Local Similarity 70.0%; Pred. No. 4.4e-05;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 NNTTGVFGLKQDWGATIKD 20
 III IIIIIIIII: I :
 Db 60 nttvgvfglkqndgdsalsn 79
 RESULT 12
 AAU04193
 ID AAU04193 standard; Protein: 280 AA.
 XX
 AC AAU04193;
 XX
 DT 23-OCT-2001 (first entry)
 XX

DE Major antigenic protein 1 (MAP1) from Ehrlichia chaffeensis.
 XX
 KW Major antigenic protein 1; MAP1; vaccine; immunogenic; rickettsia;
 KW infection; heartwater; diagnostic.
 XX
 OS Ehrlichia chaffeensis.
 XX
 PN US6251872-B1.
 XX
 PD 26-JUN-2001.
 XX
 PF 17-OCT-1997; 97US-0953326.
 XX
 PR 17-OCT-1996; 96US-0733230.
 XX
 PA (UYFL) UNIV FLORIDA.
 XX
 PI Barbet AF, Ganta RR, McGuire TC, Burridge MJ, Nyika A;
 PI Rurangirwa FR, Mahan SM, Bowie MV, Alleman AR;
 XX
 DR WPI: 2001-424487/45.
 DR N-PSDB; AAS07576.
 XX
 PT New MAP2 genes and polypeptides useful as vaccines for conferring
 PT immunity to human and animal rickettsial diseases, e.g. heartwater, or
 PT as molecular markers in nucleic acid analysis procedures
 XX
 PS Disclosure; Column 15-17; 30pp; English.
 XX
 CC The sequence represents the amino acid sequence of major antigenic
 CC protein 1 (MAP1) from Ehrlichia chaffeensis. The MAP polynucleotides and
 CC polypeptides are useful as vaccines for conferring immunity to rickettsia
 CC infection, including Cowdria ruminantium causing heartwater. The MAP
 CC polynucleotides may be used as molecular markers in nucleic acid
 CC analysis procedures, and to produce the MAP polypeptides, which may
 CC be used to raise antibodies that are reactive with the polypeptides.
 CC The nucleic acids may further be used as probes to identify
 CC complementary sequences within other nucleic acid molecules or genomes,
 CC where such probes can be applied to identify or distinguish infectious
 CC strains of organisms in diagnostic procedures or in rickettsial
 CC research where identification of particular organisms or strains is
 CC needed.
 XX
 SQ Sequence 280 AA;
 Query Match 74.5%; Score 82; DB 22; Length 280;
 Best Local Similarity 70.0%; Pred. No. 4.4e-05;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 NNTTGVFGLKQDWGATIKD 20
 III IIIIIIIII: I :
 Db 60 nttvgvfglkqndgdsalsn 79
 RESULT 13
 AAY06943
 ID AAY06943 standard; Protein: 281 AA.
 XX
 AC AAY06943;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE E. chaffeensis OMP-1 protein.
 XX
 KW Outer membrane protein; OMP; Ehrlichia chaffeensis; E. canis; P30;
 KW detection; dog.
 XX
 OS Ehrlichia chaffeensis.
 XX
 PN W09913720-A1.
 XX
 PD 25-MAR-1999.

XX 18-SEP-1998; 98WO-US19600.

XX WPI; 1999-254290/21.

XX N-PSDB; AAX34743.

XX (OHIS) UNIV OHIO STATE.

XX Ohashi N, Rikihisa Y;

XX WPI; 1999-254290/21.

XX N-PSDB; AAX34743.

XX Novel outer membrane proteins from Ehrlichia chaffeensis and

XX Ehrlichia canis

XX Disclosure; Fig 3B; 55pp; English.

XX The invention provides isolated outer membrane proteins (OMP) from

XX Ehrlichia chaffeensis and E. canis. The E. chaffeensis proteins form part

XX of the OMP family and consist of proteins OMP-1, -1(B to 2) shown

XX in AAY06943-958. The E. canis proteins form part of the P30 family and

XX consist of proteins shown in AAY06959-970. The proteins and genes are

XX used to detect E. chaffeensis in patients and E. canis in dogs.

XX Sequence 281 AA;

QY 1 NTUTGVFGLKQDWDGATIKD 20

DB 59 nttvgvfglkqndwgsalsn 78

RESULT 14

AAY06962

ID AAY06962 standard; Protein; 280 AA.

AC AAY06962;

DT 05-JUL-1999 (first entry).

DE E. canis P30-2 protein.

XX Outer membrane protein; OMP; Ehrlichia chaffeensis; E. canis; P30;

XX detection; dog.

XX Ehrlichia canis.

XX WO9913720-A1.

XX 25-MAR-1999.

XX 18-SEP-1998; 98WO-US19600.

XX 19-SEP-1997; 97US-0059353.

XX (OHIS) UNIV OHIO STATE.

XX Ohashi N, Rikihisa Y;

XX WPI; 1999-254290/21.

XX N-PSDB; AAX34762.

XX Novel outer membrane proteins from Ehrlichia chaffeensis and

XX Ehrlichia canis

XX Disclosure; Fig 2B; 55pp; English.

XX The invention provides isolated outer membrane proteins (OMP) from

XX Ehrlichia chaffeensis and E. canis. The E. chaffeensis proteins form part

CC of the OMP family and consist of proteins OMP-1, -1(B to 2) shown

CC in AAY06943-958. The E. canis proteins form part of the P30 family and

CC consist of proteins shown in AAY06959-970. The proteins and genes are

CC used to detect E. chaffeensis in patients and E. canis in dogs.

XX Sequence 280 AA;

QY 1 NTUTGVFGLKQDWDGATIKD 20

DB 59 nstvgvfglkndwngtln 78

RESULT 15

AAY71479

ID AAY71479 standard; Protein; 280 AA.

AC AAY71479;

DT 12-OCT-2000 (first entry)

DE Ehrlichia canis immunoreactive protein ECA28SA3.

XX Homologous 28-kDa protein gene; ECA28SA3; immunoreactive; vaccine;

XX P28 gene; polymorphic multiple gene family; immunoprotective antigen;

XX antibacterial; canine ehrlichiosis; canine tropical pancytopenia;

XX tick-borne rickettsial disease; serodiagnosis.

XX Ehrlichia canis.

XX Key Location/Qualifiers

FT Peptide 1..23

FT /label= Signal_peptide

FT Protein 24..280

FT /label= Mature_ECA28SA3_28-kDa_protein

XX WO200032745-A2.

XX 08-JUN-2000.

XX 24-NOV-1999; 99WO-US28075.

XX 30-NOV-1998; 98US-0201458.

XX 03-MAR-1999; 99US-0261358.

XX (RERE-) RES DEV FOUND.

XX Walker DH, Yu X, McBride JW;

XX WPI; 2000-412298/35.

XX N-PSDB; AAD01294, AAD01295.

XX Ehrlichia canis antigens useful for vaccinating against canine

XX ehrlichiosis in dogs

XX Claim 12; Page 68-69; 86pp; English.

XX The patent relates to homologous 28-kilodalton (kDa) protein genes of

XX Ehrlichia canis, designated ECA28SA1, ECA28SA2, ECA28SA3, ECA28-1 and

XX ECA28-2. These genes are members of a polymorphic multiple gene family

XX and contained in a single locus of 5.592 kb. The 28-kDa proteins are

XX immunoreactive with anti-E. canis serum hence are important

XX immunoprotective antigens. The protein is useful for vaccinating

XX against E. canis infections such as canine ehrlichiosis in dogs.

XX Canine ehrlichiosis, also known as canine tropical pancytopenia, is a

XX tick-borne rickettsial disease of dogs. ECA28-1 is conserved amongst

XX different strains of E. canis and hence useful for serodiagnosis of

XX canine ehrlichiosis. The present sequence is a E. canis

XX ECA28SA3 30-kDa protein which is post-translationally modified to a

CC mature 28-kDa protein by cleavage of N-terminal signal sequence.

XX

SQ Sequence 280 AA;

Query Match 70.0%; Score 77; DB 21; Length 280;
Best Local Similarity 65.0%; Pred. No. 0.00028;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 NTTGVFGLKQDWGATIKD 20

|:| ||||| ||:| |:
Db 59 nstvgvfglxhdwnggtlsp 78

Search completed: June 7, 2002, 14:30:16
Job time: 558 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2002, 14:27:08 ; Search time 13.08 seconds
(without alignments)
37.348 Million cell updates/sec

Title: US-10-054-647-2

Perfect score: 110

Sequence: 1 NTTTGVFLKQDWDGATIKD 20

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000.

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*

3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*

4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*

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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	81.8	280	4	US-08-953-326-17
2	82	74.5	276	4	US-08-953-326-18
3	82	74.5	280	3	US-08-733-230-4
4	82	74.5	280	4	US-08-953-326-4
5	71	64.5	286	4	US-08-953-326-15
6	59.5	54.1	287	3	US-08-733-230-2
7	59.5	54.1	287	4	US-08-953-326-2
8	59	53.6	278	4	US-08-953-326-16
9	49	44.5	133	4	US-08-953-326-20
10	40.5	36.8	1025	2	US-08-304-309-2
11	40.5	36.8	1025	3	US-08-991-942-2
12	40.5	36.8	1025	4	US-09-138-103-2
13	40.5	36.8	1025	5	PCT-US95-04567-4
14	40.5	36.8	2048	4	US-09-268-347-48
15	40	36.4	523	4	US-09-550-338-2
16	40	36.4	1212	4	US-09-268-866-2
17	39	35.5	182	3	US-08-828-741B-2
18	39	35.5	182	4	US-09-160-567-2
19	39	35.5	1025	2	US-08-304-309-4
20	39	35.5	1025	3	US-08-991-942-4
21	39	35.5	1025	5	PCT-US95-04567-2
22	38.5	35.0	569	2	US-08-467-822-27
23	38.5	35.0	569	4	US-08-432-697-27
24	38.5	35.0	569	4	US-08-466-248-27
25	38.5	35.0	859	1	US-08-053-614-2
26	38.5	35.0	859	1	US-08-316-397B-2
27	38.5	35.0	859	2	US-09-034-306-2

28 38.5 35.0 859 4 US-09-259-437-2 Sequence 2, Appli
29 38.5 35.0 859 5 PCT-US93-09782-2 Sequence 2, Appli
30 38.5 35.0 1181 1 US-08-053-614-4 Sequence 4, Appli
31 38.5 35.0 1181 1 US-08-316-397B-4 Sequence 4, Appli
32 38.5 35.0 1181 2 US-09-034-306-4 Sequence 4, Appli
33 38.5 35.0 1181 4 US-09-259-437-4 Sequence 4, Appli
34 38.5 35.0 1181 5 PCT-US93-09782-4 Sequence 4, Appli
35 38 34.5 135 1 US-08-446-600A-4 Sequence 4, Appli
36 38 34.5 247 4 US-09-199-637A-363 Sequence 363, App
37 38 34.5 338 4 US-09-413-231-6 Sequence 6, Appli
38 38 34.5 338 4 US-09-413-231-7 Sequence 7, Appli
39 38 34.5 371 3 US-08-586-165-3 Sequence 3, Appli
40 38 34.5 372 3 US-08-586-165-5 Sequence 5, Appli
41 38 34.5 548 1 US-08-333-358-2 Sequence 2, Appli
42 38 34.5 548 1 US-08-463-694-2 Sequence 2, Appli
43 38 34.5 548 1 US-08-694-501-2 Sequence 2, Appli
44 37.5 34.1 536 4 US-08-426-509A-12 Sequence 12, Appli
45 37.5 34.1 536 5 PCT-US95-05008-12 Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-08-953-326-17
; Sequence 17, Application US/089533326
; Patent No. 6251872
; GENERAL INFORMATION:
; APPLICANT: Barbet, Anthony F.
; APPLICANT: Ganta, Roman R.
; APPLICANT: McGuire, Travis C.
; APPLICANT: Burridge, Michael J.
; APPLICANT: Nyika, Aceme
; APPLICANT: Rurangirwa, Fred R.
; APPLICANT: Mahan, Suman M.
; TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
; FILE REFERENCE: UP-167C1
; CURRENT APPLICATION NUMBER: US/08/953,326
; CURRENT FILING DATE: 1997-10-17
; EARLIER APPLICATION NUMBER: 08/953,326
; EARLIER FILING DATE: 1997-10-17
; EARLIER APPLICATION NUMBER: 08/733,230
; EARLIER FILING DATE: 1996-10-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-17

Query Match 81.8%; Score 90; DB 4; Length 280;
Best Local Similarity 88.9%; Pred. No. 4.9e-07;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NTTTGVFLKQDWDGATIK 18

DB 60 NTTTGVFLKQDWDGATIK 77

RESULT 2

US-08-953-326-18
; Sequence 18, Application US/089533326
; Patent No. 6251872
; GENERAL INFORMATION:
; APPLICANT: Barbet, Anthony F.
; APPLICANT: Ganta, Roman R.
; APPLICANT: McGuire, Travis C.
; APPLICANT: Burridge, Michael J.
; APPLICANT: Nyika, Aceme
; APPLICANT: Rurangirwa, Fred R.

APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
Animals and Humans
FILE REFERENCE: UF-167C1
CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/733,230
EARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ. ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 276
TYPE: PRT
ORGANISM: Ehrlichia chaffeensis
US-08-953-326-18

Query Match 74.5%; Score 82; DB 4; Length 276;
Best Local Similarity 70.0%; Pred. No. 9.5e-06;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 NTTGVFGLKQDWDGATIKD 20
DB 59 NTTGVFGLKQDWDGSAISN 78

RESULT 3
US-08-733-230-4
Sequence 4, Application US/08/733230
Patent No. 6025338
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: McGuire, Travis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Nyika, Aceme
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against
Rickettsial Diseases and Methods of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,230
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF-167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-733-230-4

Query Match 74.5%; Score 82; DB 3; Length 280;
Best Local Similarity 70.0%; Pred. No. 9.6e-06;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 NTTGVFGLKQDWDGATIKD 20
DB 60 NTTGVFGLKQDWDGSAISN 79

RESULT 4
US-08-953-326-4
Sequence 4, Application US/08953326
Patent No. 6251872
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: McGuire, Travis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Nyika, Aceme
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
Animals and Humans
FILE REFERENCE: UF-167C1
CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/733,230
EARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 280
TYPE: PRT
ORGANISM: Ehrlichia chaffeensis
US-08-953-326-4

Query Match 74.5%; Score 82; DB 4; Length 280;
Best Local Similarity 70.0%; Pred. No. 9.6e-06;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 NTTGVFGLKQDWDGATIKD 20
DB 60 NTTGVFGLKQDWDGSAISN 79

RESULT 5
US-08-953-326-15
Sequence 15, Application US/08953326
Patent No. 6251872
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: McGuire, Travis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Nyika, Aceme
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
Animals and Humans
FILE REFERENCE: UF-167C1
CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/733,230
EARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0

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; SEQ ID NO 15
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-15

Query Match      64.5%; Score 71; DB 4; Length 286;
Best Local Similarity 66.7%; Pred. No. 0.00059;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 NTTTGVFLKQDWDGAI 18
Db 60 NTTTGVFLKQDWDRCVI 77

RESULT 6
US-08-733-230-2
; Sequence 2, Application US/08733230
; Patent No. 6025338
; GENERAL INFORMATION:
; APPLICANT: Barbet, Anthony F.
; APPLICANT: Ganta, Roman R.
; APPLICANT: McGuire, Travis C.
; APPLICANT: Burridge, Michael J.
; APPLICANT: Nyika, Aceme
; APPLICANT: Rurangirwa, Fred R.
; APPLICANT: Mahan, Suman M.
; TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,230
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF-167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-733-230-2

Query Match      54.1%; Score 59.5; DB 3; Length 287;
Best Local Similarity 80.0%; Pred. No. 0.043;
Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 NTTTGVFLKQDWDG 15
Db 62 NTQT-VFGLKQDWDG 75

RESULT 7
US-08-733-230-2
; Sequence 2, Application US/08733230
; Patent No. 6025338
; GENERAL INFORMATION:
; APPLICANT: Barbet, Anthony F.
; APPLICANT: Ganta, Roman R.
; APPLICANT: McGuire, Travis C.
; APPLICANT: Burridge, Michael J.
; APPLICANT: Nyika, Aceme
; APPLICANT: Rurangirwa, Fred R.
; APPLICANT: Mahan, Suman M.
; TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,230
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF-167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-733-230-2

Query Match      54.1%; Score 59.5; DB 4; Length 287;
Best Local Similarity 80.0%; Pred. No. 0.043;
Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 NTTTGVFLKQDWDG 15
Db 62 NTQT-VFGLKQDWDG 75

RESULT 8
US-08-953-326-16
; Sequence 16, Application US/08953326
; Patent No. 6251872
; GENERAL INFORMATION:
; APPLICANT: Barbet, Anthony F.
; APPLICANT: Ganta, Roman R.
; APPLICANT: McGuire, Travis C.
; APPLICANT: Burridge, Michael J.
; APPLICANT: Nyika, Aceme
; APPLICANT: Rurangirwa, Fred R.
; APPLICANT: Mahan, Suman M.
; TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
; FILE REFERENCE: UF-167C1
; CURRENT APPLICATION NUMBER: US/08/953,326
; CURRENT FILING DATE: 1997-10-17
; EARLIER APPLICATION NUMBER: 08/953,326
; EARLIER FILING DATE: 1997-10-17
; EARLIER APPLICATION NUMBER: 08/733,230
; EARLIER FILING DATE: 1996-10-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-16

Query Match      53.6%; Score 59; DB 4; Length 278;
Best Local Similarity 60.0%; Pred. No. 0.05;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 NTTTGVFLKQDWDG 15
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US-08-953-326-2
; Sequence 2, Application US/08953326
; Patent No. 6251872
; GENERAL INFORMATION:
; APPLICANT: Barbet, Anthony F.
; APPLICANT: Ganta, Roman R.
; APPLICANT: McGuire, Travis C.
; APPLICANT: Burridge, Michael J.
; APPLICANT: Nyika, Aceme
; APPLICANT: Rurangirwa, Fred R.
; APPLICANT: Mahan, Suman M.
; TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
; FILE REFERENCE: UF-167C1
; CURRENT APPLICATION NUMBER: US/08/953,326
; CURRENT FILING DATE: 1997-10-17
; EARLIER APPLICATION NUMBER: 08/953,326
; EARLIER FILING DATE: 1997-10-17
; EARLIER APPLICATION NUMBER: 08/733,230
; EARLIER FILING DATE: 1996-10-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Cowdria ruminantium
US-08-953-326-2

Query Match      54.1%; Score 59.5; DB 4; Length 287;
Best Local Similarity 80.0%; Pred. No. 0.043;
Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 NTTTGVFLKQDWDG 15
Db 62 NTQT-VFGLKQDWDG 75

RESULT 8
US-08-953-326-16
; Sequence 16, Application US/08953326
; Patent No. 6251872
; GENERAL INFORMATION:
; APPLICANT: Barbet, Anthony F.
; APPLICANT: Ganta, Roman R.
; APPLICANT: McGuire, Travis C.
; APPLICANT: Burridge, Michael J.
; APPLICANT: Nyika, Aceme
; APPLICANT: Rurangirwa, Fred R.
; APPLICANT: Mahan, Suman M.
; TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
; FILE REFERENCE: UF-167C1
; CURRENT APPLICATION NUMBER: US/08/953,326
; CURRENT FILING DATE: 1997-10-17
; EARLIER APPLICATION NUMBER: 08/953,326
; EARLIER FILING DATE: 1997-10-17
; EARLIER APPLICATION NUMBER: 08/733,230
; EARLIER FILING DATE: 1996-10-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-16

Query Match      53.6%; Score 59; DB 4; Length 278;
Best Local Similarity 60.0%; Pred. No. 0.05;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 NTTTGVFLKQDWDG 15
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; LENGTH: 1025 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04567-4

Query Match          36.8%   Score 40.5;   DB 5;   Length 1025;
Best-Local Similarity 42.9%;   Pred.No. 2.2e+02;
Matches 9; Conservative 2; Mismatches 7; Indels 3

QY      1  NNTTGVFLKQD---WDGATI 18
      II : I: I I I I I I I
Db      736  NTVSGLMGLKSDGTPWPAVG 756

RESULT 14
US-09-268-347-48
; Sequence 48, Application US/09268347
; Patent No. 6335182
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN
; FILE REFERENCE: 1038-860
; CURRENT APPLICATION NUMBER: US/09/268.347
; CURRENT FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 54.
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 2048
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-268-347-48

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Query Match          36.8%; Score 40.5; DB 4; Length 2048;
Best Local Similarity 39.3%; Pred. No. 5e+02;
Matches 11; Conservative 1; Mismatches 5; Indels 11; Gaps 1;

QY      .4 TGVEGLKQDW-----DGATIKD 20
      |  ||| ||
DB      686 TVTFGLSQDSGLTGKSTLNNDGLTVKD 713

RESULT 15
US-09-550-338-2
; Sequence 22, Application US/09550338
; Patent No. 6210951
; GENERAL INFORMATION:
; APPLICANT: KAWASAKI, Hisashi
; APPLICANT: USUDA, Yoshihiro
; APPLICANT: MIHARA, Yoshihiro
; APPLICANT: KURAHASHI, Osamu
; TITLE OF INVENTION: GMP Synthetase and Gene Coding for the Same
; FILE REFERENCE: 0010-1101-0
; CURRENT APPLICATION NUMBER: US/09/550,338
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: JP 11-114787
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Brevibacterium lactofermentum (Corneybacterium glutamicum)
US-09-550-338-2

Query Match          36.4%; Score 40; DB 4; Length 523;
Best Local Similarity 41.2%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      4 TGVEGLKQDWDGATIKD 20

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Db 190 TEIAGLEQNTAANIAE 206

Search completed: June 7, 2002, 14:30:36
Job time: 206 sec

GenCore version 4.5
Copyright (c) 1993-2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2002, 14:27:58, Search time 15.01 Seconds
(without alignments)
128.034 Million cell updates/sec

Title: US-10-054-647-2

Perfect score: 110
Sequence: 1 NTTVGVFLKQDWDGATIKD 20

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 71.1*

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	90	81.8	280	2 JE0217	28k surface antige
2	82	74.5	276	2 JE0218	28k surface antige
3	71	64.5	286	2 JE0219	28k surface antige
4	59	53.6	278	2 JE0216	28k surface antige
5	59	53.6	284	2 I40882	major antigenic pr
6	52	47.3	5188	2 B85547	probable RIX fami
7	52	47.3	5291	2 F90696	hypothetical prote
8	51	46.4	1191	2 A53491	bumetanide-sensiti
9	49	44.5	133	2 JE0221	28k surface antige
10	49	44.5	634	2 F97172	flagellar hook-ass
11	47	42.7	540	2 S54586	probable membrane
12	47	42.7	584	2 C48558	flagellin - Escher
13	46.5	42.3	287	2 C83242	conserved hypothet
14	46	41.8	261	2 G84057	hypothetical prote
15	45	40.9	160	2 A75466	2-demethylmenagui
16	45	40.9	756	2 T20109	hypothetical prote
17	44	40.0	281	2 AH3012	outer surface prot
18	44	40.0	284	2 B69945	phage-related prot
19	44	40.0	284	2 G98271	hypothetical prote
20	44	40.0	465	1 S47738	cytochrome-c perox
21	44	40.0	465	2 F91178	cytochrome-c perox
22	44	40.0	465	2 G86024	cytochrome-c perox
23	44	40.0	534	2 C82096	aminoacyl-histidin
24	44	40.0	648	1 P3BFF6	F3 protein - phage
25	44	40.0	1004	2 JH0470	Na+/K+-exchanging
26	43.5	39.5	290	2 S76787	hypothetical prote
27	43	39.1	280	2 D70976	hypothetical prote
28	43	39.1	437	2 I40167	dihydroorotase (EC
29	43	39.1	470	2 JC4098	tetracycline 6-hyd

ALIGNMENTS

RESULT 1

JE0217
28k surface antigen 4 - Ehrlichia chaffensis
N: Alternate names: MAP1
C: Species: Ehrlichia chaffensis
C: Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
C: Accession: JE0217
R: Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A: Title: Molecular characterization of a 28kDa surface antigen gene family of the tri
A: Reference number: JE0216; MUID:98321180
A: Accession: JE0217
A: Molecule type: DNA
A: Residues: 1-280 <RED>
A: Cross-references: GB:AF062761

Query Match 81.8%; Score 90; DB 2; Length 280;
Best Local Similarity 88.9%; Pred. No. 1.8e-06;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NTTVGVFLKQDWDGATI 18
DB 60 NTTVGVFLKQDWDGSTI 77
|||||

RESULT 2

JE0218
28k surface antigen 5 - Ehrlichia chaffensis
N: Alternate names: MAP1
C: Species: Ehrlichia chaffensis
C: Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
C: Accession: JE0218
R: Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A: Title: Molecular characterization of a 28kDa surface antigen gene family of the tri
A: Reference number: JE0216; MUID:98321180
A: Accession: JE0218
A: Molecule type: DNA
A: Residues: 1-276 <RED>
A: Cross-references: GB:AF062761

Query Match 74.5%; Score 82; DB 2; Length 276;
Best Local Similarity 70.0%; Pred. No. 3.1e-05;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 NTTVGVFLKQDWDGATIKD 20
DB 59 NTTVGVFLKQDWDGSAIN 78
|||||

probable leucyl am
hypothetical prote
Na+/K+-exchanging
hypothetical prote
rhizobioicin/RTX to
probable phosphoes
conserved hypothet
hypothetical prote
hypothetical prote
probable formate a
probable activatin
probable activatin
hypothetical prote
S-adenosylmethionin
conserved hypothet
dnaA protein - Str

30 43 39.1 482 2 G75483
31 43 39.1 681 2 G87276
32 43 39.1 1037 2 A56594
33 43 39.1 1649 2 C86822
34 43 39.1 1944 2 AH3098
35 43 39.1 1990 2 A96188
36 42.5 38.6 123 2 AE0293
37 42 38.2 160 2 A12476
38 42 38.2 224 2 C72390
39 42 38.2 287 1 S56603
40 42 38.2 287 2 A91296
41 42 38.2 287 2 D86137
42 42 38.2 307 2 T44893
43 42 38.2 362 2 F75379
44 42 38.2 413 2 T08297
45 42 38.2 656 2 A41870

RESULT 3
 JEO219
 28k surface antigen 2 - Ehrlichia chaffensis
 N:Alternate names: MAP1
 C:Species: Ehrlichia chaffensis
 C>Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
 C:Accession: JEO219
 R:Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
 Biochem. Biophys. Res. Commun. 247, 636-643, 1998
 A:Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe
 A:Reference number: JEO216; MUID:98321180
 A:Accession: JEO219
 A:Molecule type: DNA
 A:Residues: 1-286 <RED>
 A:Cross-references: GB:AF062761

Query Match 64.5%; Score 71; DB 2; Length 286;
 Best Local Similarity 66.7%; Pred. No. 0.0017;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 NTTGVFGLKQDWDGAT 18
 ||| ||||:|||||
 Db : 60 NTTGVFGLKQDWDRCV 77

RESULT 4
 JEO216
 28k surface antigen 3 - Ehrlichia chaffensis
 N:Alternate names: MAP1
 C:Species: Ehrlichia chaffensis
 C>Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
 C:Accession: JEO216
 R:Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
 Biochem. Biophys. Res. Commun. 247, 636-643, 1998
 A:Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe
 A:Reference number: JEO216; MUID:98321180
 A:Accession: JEO216
 A:Molecule type: DNA
 A:Residues: 1-278 <RED>
 A:Cross-references: GB:AF062761

Query Match 53.6%; Score 59; DB 2; Length 278;
 Best Local Similarity 60.0%; Pred. No. 0.12;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 NTTGVFGLKQDWDG 15
 . | | : ||||| |
 Db 60 NPTVALYGLKQDWDG 74

RESULT 5
 I40882
 major antigenic protein - heartwater rickettsia
 C:Species: Cowdria ruminantium (heartwater rickettsia)
 C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
 C:Accession: I40882; S42827
 R:van Vliet, A.H.; Jongejan, F.; van Kleef, M.; van der Zeijst, B.A.
 Infect. Immun. 62, 1451-1456, 1994
 A:Title: Molecular cloning, sequence analysis, and expression of the gene encoding the
 A:Reference number: I40882; MUID:94178956
 A:Accession: I40882
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-284 <RES>
 A:Cross-references: EMBL:X74250; NID:G454266; PIDN:CAA52309.1; PID:G454267
 C:Genetics:
 A:Gene: map1

Query Match 53.6%; Score 59; DB 2; Length 284;
 Best Local Similarity 76.9%; Pred. No. 0.13;

Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTGVFGLKQDWDG 15
 | ||||| ||||
 Db 63 TKAVFGLKQDWDG 75

RESULT 6
 B85547
 probable RTX family exoprotein [imported] - Escherichia coli (strain O157:H7, substra
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: B85547
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
 iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: B85480; MUID:21074935; PMID:11206551
 A:Accession: B85547
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-5188 <STO>
 A:Cross-references: GB:AE005174; NID:G12513368; PIDN:AAG54838.1; GSPDB:GN00145; UWGP:
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: Z0615

Query Match 47.3%; Score 52; DB 2; Length 5188;
 Best Local Similarity 60.0%; Pred. No. 37;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 TTGVFGLKQDWDGA 16
 ||| | : |||||
 Db 4803 TTSGVAAMDYDWDGA 4817

RESULT 7
 F90696
 hypothetical protein ECs0542 [imported] - Escherichia coli (strain O157:H7, substrain
 C:Species: Escherichia coli
 C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
 C:Accession: F90696
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: F90696
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-5291 <HAV>
 A:Cross-references: GB:BA000007; PIDN:BA033965.1; PID:G13360000; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RMD 0509952
 C:Genetics:
 A:Gene: ECs0542

Query Match 47.3%; Score 52; DB 2; Length 5291;
 Best Local Similarity 60.0%; Pred. No. 38;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 TTGVFGLKQDWDGA 16
 ||| | : |||||
 Db 4906 TTSGVAAMDYDWDGA 4920

RESULT 8
 A53491
 bumetanide-sensitive Na-K-Cl cotransporter - spiny dogfish
 C:Species: Squalus acanthias (spiny dogfish)
 C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 02-Mar-2001
 C:Accession: A53491

0v 1 NTTGVFGLKODWDGATTKD 20

DB, 109 NTTTGLVGLKTF 210

RESULT 13

C83242
conserved hypothetical protein PA3239 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83242
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V...
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337
A:Accession: C83242
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-267 <STO>
A:Cross-references: GB:AE004746; GB:AE004091; NID:g9949350; PIDN:AAG06627.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3239

Query Match 42.3%; Score 46.5; DB 2; Length 267;
Best Local Similarity 64.7%; Pred. No. 11;
Matches 11; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 1 NTGTGFGFLKQDWDGAT 17
||| || || || || ||
DB 145 NTGTGVLGL---WDPAT 158

RESULT 14

G84057
hypothetical protein BH3263 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: G84057
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: G84057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-261 <STO>
A:Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB06982.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3263
C:Superfamily: Bacillus subtilis hypothetical protein ytmp

Query Match 41.8%; Score 46; DB 2; Length 261;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 DWDCATKID 20
||||| |
DB 177 DWDCATVAD 185

RESULT 15

A75466
2-demethylmenaquinone 2-C-methyltransferase (EC 2.1.1.-) DR0859 [similarity] - Deinococ
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Sep-2000
C:Accession: A75466
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zaleski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: A75466

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-160 <WHI>
A:Cross-references: GB:AE001940; GB:AE000513; NID:g6458577; PIDN:AAF10437.1; PID:g645
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0859
A:Map position: 1
C:Keywords: methyltransferase

Query Match 40.9%; Score 45; DB 2; Length 160;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 GVFGFKQDWDGATI 18
||||| |
DB 80 GVFGVNGWEGVII 93

Search completed: June 7, 2002, 14:30:58
Job time: 180 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2002, 14:30:38 Search time 10.34 Seconds
(without alignments)
74.893 Million cell updates/sec

Title: US-10-054-647-2

Perfect score: 110

Sequence: 1 NITTVGLKQWDGATKD 20

Scoring table: BLOSUM62
Gapop 10.0 Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	46.4	1191	1	NCCL_SQUAC
2	47	42.7	540	1	Y8M_YEAST
3	45	40.9	160	1	MENG_DEIRA
4	45	40.9	756	1	K6PF_CABEL
5	44	40.0	284	1	YQAK_BACSU
6	44	40.0	465	1	YHJA_ECOLI
7	44	40.0	648	1	VP3_BPRH6
8	44	40.0	1004	1	ATIA_ARTSF
9	43.5	39.5	230	1	AROE_SYNY3
10	43	39.1	427	1	PYRC_BACCL
11	43	39.1	1021	1	ALAI_CANFA
12	42	38.2	287	1	XJW_ECOLI
13	42	38.2	307	1	YM16_MYLE
14	42	38.2	656	1	DNAI_SIRCO
15	42	38.2	1020	1	ALAI_HUMAN
16	41.5	37.7	366	1	GCST_NEIMB
17	41.5	37.7	368	1	GCST_NEIMA
18	41	37.3	377	1	YA67_METH
19	41	37.3	395	1	KIME_RAT
20	41	37.3	684	1	HP4_PORGI
21	41	37.3	749	1	VRG_ROTAVI
22	41	37.3	866	1	YCBS_ECOLI
23	40.5	36.8	196	1	ANFL_CHICK
24	40.5	36.8	734	1	PURL_ZYMO
25	40.5	36.8	1025	1	DPYD_HUMAN
26	40	36.4	84	1	GWML_HALN1
27	40	36.4	120	1	YRAJ_BACSU
28	40	36.4	191	1	PGHD_URSA
29	40	36.4	282	1	BIOB_HELPJ
30	40	36.4	282	1	BIOB_HELPJ
31	40	36.4	341	1	X33B_MYCPN
32	40	36.4	489	1	UBPT_CABEL
33	40	36.4	500	1	AMPA_BACSU

34 40 36.4 942 1 ENV_CAEVG
35 40 36.4 1020 1 AIA2_RAT
36 40 36.4 1023 1 AIA1_HUMAN
37 40 36.4 1041 1 ATNA_DROME
38 40 36.4 1205 1 NKCI_MOUSE
39 40 36.4 1212 1 NKCI_HUMAN
40 40 36.4 1295 1 GLPI_CAEEL
41 40 36.4 1429 1 LII2_CAEEL
42 39 35.5 105 1 YGRM_MICEC
43 39 35.5 118 1 ANFD_RANCA
44 39 35.5 149 1 DTD_CLOAB
45 39 35.5 267 1 NUSL_ASPOR

ALIGNMENTS

RESULT 1
NCCL_SQUAC STANDARD PRT: 1191 AA.
AC P55013;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Bimetanide-sensitive sodium-(Potassium)-chloride cotransporter 1
DE (NA-K-CL symporter) (NKCC).
GN SLC12A2 OR NKCC1.
OS Squallus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE FROM N.A., AND PHOSPHORYLATION SITES.
RC TISSUE=Rectal gland;
RX MEDLINE=94181560; PubMed=813473;
RA Xu J.-C., Lytle C., Zhu T.T., Payne J.A., Benz E. Jr., Forbush B. III;
RT "Molecular cloning and functional expression of the
bimetanide-sensitive Na-K-Cl cotransporter."
RL Proc. Natl. Acad. Sci. U.S.A. 91:2201-2205(1994).
CC -I- FUNCTION: ELECTRICALLY SILENT TRANSPORTER SYSTEM WHICH IS A
MEDIATOR OF SODIUM AND CHLORIDE REABSORPTION. PLAYS A VITAL ROLE
IN THE REGULATION OF IONIC BALANCE AND CELL VOLUME.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES.
CC -I- SIMILARITY: BELONGS TO THE SLC12A FAMILY OF TRANSPORTERS.
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EMBL; U05958; AAB60617.1;
DR InterPro; IPR002293; AA_rel_permease.1.
DR InterPro; IPR002027; Amino_acid_permease.
DR InterPro; IPR002443; NaKCl_transporter.
DR Pfam; PF00324; aa_permeases.1.
DR PRINTS; PR01207; NAKCLTRNSPT.
KW Transport; Transmembrane; Glycoprotein; Phosphorylation.
FT DOMAIN 1 257 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 258 278 POTENTIAL.
FT DOMAIN 279 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 302 POTENTIAL.
FT DOMAIN 303 339 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 340 360 POTENTIAL.
FT DOMAIN 361 382 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 383 403 POTENTIAL.
FT DOMAIN 404 407 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 408 428 POTENTIAL.
FT DOMAIN 429 458 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 459 479 POTENTIAL.

QY 5 GVFGKQDWGATIK 18
| | | | |
Db 80 GVFGWENGWGVII 93

RESULT 4
KQPF_CAEEL
ID KQPF_CAEEL STANDARD; PRT; 756 AA.
AC Q27483;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
DE (Phosphohexokinase)
GN C50F4.2
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL-N2;
RA Murray A.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate -> ADP + D-fructose 1,6-bisphosphate;
CC -1- PATHWAY: KEY CONTROL STEP OF GLYCOLYSIS.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOFRUCTOKINASE FAMILY, TWO DOMAIN SUBFAMILY.
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DR EMBL; Z70750; CAA94737.1;
DR HSSP; P00512; 3PFK.
DR InterPro; C50F4.2; CE05467.
DR InterPro; IPR000023; Phosphofructokinase.
DR Pfam; PF00365; PFK; 2.
DR PRINTS; PR00476; PFKCTKINASE.
DR ProDom; PD000707; Phosphofructokinase; 2.
DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
KW Kinase; Transferase; Glycolysis; Repeat.
SQ SEQUENCE 756 AA; 83301 MW; 26A89B801D286534 CRC64;

Query Match 40.9%; Score 45; DB 1; Length 756;
Best Local Similarity 53.3%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 VEGKQDWGATIKD 20
| | | | |
Db 436 VIGKHGWDGLKND 450

RESULT 5
YQAK_BACSU
ID YQAK_BACSU STANDARD; PRT; 284 AA.
AC P45908;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 32.2 kDa protein in SPOIIC-CMLA intergenic region.
GN YQAK
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-168 / JH642;
RX MEDLINE-95219086; PubMed-7704261;
RA Takemaru K.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi Y.;
RT "Complete nucleotide sequence of a skin element excised by DNA rearrangement during sporulation in *Bacillus subtilis*.";
RL Microbiology 141:323-327(1995).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN-168 / JH642;
RA Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S., Sato T.,
RA Takeuchi M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]

RP IDENTIFICATION.
RX MEDLINE-96084975; PubMed-7489895;
RA Medigue C., Moszer I., Viari A., Danchin A.;
RT "Analysis of a *Bacillus subtilis* genome fragment using a co-operative computer system prototype.";
RL Gene 165:GC37-GC51(1995).
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DR EMBL; D32216; BAA06925.1;
DR EMBL; D84432; BAA12386.1;
DR EMBL; Z99117; CAB14569.1;
DR Subtilist; BG11262; Yqak.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 284 AA; 32170 MW; F255261D4692ADB7 CRC64;

Query Match 40.0%; Score 44; DB 1; Length 284;
Best Local Similarity 53.8%; Pred. No. 6.7;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 7 FGLKQDWGATIK 19
| | | | |
Db 193 FGKNDWDAMALK 205

RESULT 6
YHJA_ECOLI
ID YHJA_ECOLI STANDARD; PRT; 465 AA.
AC P37197;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable cytochrome C peroxidase (EC 1.1.1.1.5).
GN YHJA OR B3518.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE-94316500; PubMed-8041620;
RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT "Analysis of the *Escherichia coli* genome. V. DNA sequence of the region from 76.0 to 81.5 minutes.";
RL Nucleic Acids Res. 22:2576-2586(1994).
CC -1- CATALYTIC ACTIVITY: 2 ferrocyclochrome c + 2 H(2)O -> ferrocyclochrome c + 2 H(2).
CC -1- PTM: BINDS 3 HEMES (POTENTIAL).
CC -1- SIMILARITY: HIGH, TO P.AERUGINOSA CYTOCHROME C551 PEROXIDASE.
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Query Match 40.0%; Score 44; DB 1; Length 648;
Best Local Similarity 41.2%; Pred. No. 16;
Matches 7; Conservative 5; Mismatches 3; Indels 2; Gaps

[illegible]

subunit." ;
Gene 105:197-204(1991).
-1- FUNCTION: THIS IS THE CATALYTIC COMPONENT OF THE ACTIVE ENZYME,

NA AND K IONS ACROSS THE PLASMA MEMBRANE. THIS ACTION CREATES IN THE CYTOSOL AN ELECTROCHEMICAL GRADIENT OF NA AND K, PROVIDING THE ENERGY FOR ACTIVE TRANSPORT OF VARIOUS NUTRIENTS.

-!- SUBUNIT: COMPOSED OF THREE SUBUNITS: ALPHA {CATALYTIC}; BETA AND GAMMA.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY IIC.

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EMBL: X56650; CAA39972.1; -
PIR: JH0470; JH0470.
HSSP: P04191; IEUL.

InterPro: IPR004014; Cation_ATPase.
InterPro: IPR001757; E1-E2_ATPase.
InterPro: IPR001454; Hydrolase.
InterPro: IPR000661; Na_H_KATPase.
Pfam: PF00689; Cation_ATPase_C; 1.

PFAM: PF00122; EL-E2 ATPase; 1.
PFAM: PF00702; Hydrolyase; 1.
PRINTS: PR00119; CATATPASE.
PRINTS: PR00121; NAKATPASE.
PROSITE: PS00154; ATPASE_E1_E2; 1.
Hydrolyase; Sodium/potassium transport; Transmembrane;
Phosphorylation; ATP-binding.

T	TRANSWEM	110	BY SIMILARITY.
T	TRANSWEM	126	BY SIMILARITY.
T	TRANSWEM	272	BY SIMILARITY.
T	TRANSWEM	294	BY SIMILARITY.
T	TRANSWEM	301	BY SIMILARITY.
T	TRANSWEM	329	BY SIMILARITY.
T	TRANSWEM	768	BY SIMILARITY.
T	TRANSWEM	791	BY SIMILARITY.

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FT TRANSHEM      828      855      BY SIMILARITY.
FT TRANSHEM      897      918      BY SIMILARITY.
FT TRANSHEM      934      959      BY SIMILARITY.
FT MOD_RES       357      357      PHOSPHORYLATION (PROBABLE).
FT BINDING       489      489      ATP (BY SIMILARITY).
SQ SEQUENCE      1004 AA; 110699 MW; C84E6BCE19A78C7 CRC64;

Query Match      40.0%; Score 44; DB 1; Length 1004;
Best Local Similarity 40.0%; Pred. No. 26;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 VFGKQDWDGATIKD 20
DB 864 LFGURKWDGRAVND 878

RESULT 9
AROE_SVNY3
ID AROE_SVNY3 STANDARD; PRT; 290 AA
AC P74591;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Shikimate 5-dehydrogenase (EC 1.1.1.25).
GN AROE OR SLR159.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97081201; PubMed=8905231;
RX Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugiyama M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
CC -1- CATALYTIC ACTIVITY: Shikimate + NADP(+) -> 5-dehydroshikimate +
CC NADPH.
CC -1- PATHWAY: FOURTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN THE
CC BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
CC -1- SIMILARITY: BELONGS TO THE SHIKIMATE DEHYDROGENASE FAMILY.
CC
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CC
CC EMBL; D90916; BAA18699.1;
CC InterPro; IPR002907; Shikimate_DH.
CC Pfam; PF01488; Shikimate_DH.1;
CC Aromatic amino acid biosynthesis; Oxidoreductase; NADP;
CC Complete proteome.
SQ SEQUENCE 290 AA; 31099 MW; 8A2D38EE5D57B303 CRC64;

Query Match      39.5%; Score 43.5; DB 1; Length 290;
Best Local Similarity 47.8%; Pred. No. 8.3;
Matches 11; Conservative 0; Mismatches 5; Indels 7; Gaps 1;

QY 2 TTTCVFG-----LKQDWDGAT 17
DB 105 TMTDVEGFLAPLLEKQDWSGRT 127

RESULT 10
ALAL_CANFA
ID ALAL_CANFA STANDARD; PRT; 1021 AA
AC P50997;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sodium/potassium-transporting ATPase alpha-1 chain precursor
DE (EC 3.6.3.9). (Sodium pump 1) (Na+/K+ ATPase 1).
GN ATP1A1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;

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PYRC_BACCL
ID PYRC_BACCL STANDARD; PRT; 427 AA
AC P46538;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dihydroorotase (EC 3.5.2.3) (DHOase).
GN PYRC.
OS Bacillus caldolyticus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1394;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=DSM 405;
RX MEDLINE=94282293; PubMed=7516791;
RA Ghim S.Y., Nielsen P., Neuhaed J.;
RT "Molecular characterization of pyrimidine biosynthesis genes from the
RT thermophile Bacillus caldolyticus."
RL Microbiology 140:479-491(1994).
CC -1- CATALYTIC ACTIVITY: (S)-dihydroorotate + H(2)O -> N-carbamoyl-L-
CC aspartate.
CC -1- COFACTOR: THIS ENZYME TIGHTLY BINDS ONE ZINC ATOM PER CHAIN WHICH
CC IS REQUIRED FOR THE CATALYTIC MECHANISM. IT ALSO BINDS WEAKLY TO
CC TWO OTHERS ZINCS WHICH ARE NOT ESSENTIAL FOR ACTIVITY
CC (BY SIMILARITY).
CC -1- PATHWAY: THIRD STEP IN PYRIMIDINE BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE DHOASE FAMILY. SUBFAMILY 2.
CC
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CC
CC EMBL; X73308; CAA51737.1;
CC MEROPS; M38.972;
CC InterPro; IPR002195; Dihydroorotase.
CC Pfam; PF00744; Dihydroorotase.1;
CC PROSITE; PS00483; DIHYDROOROTASE_1; 1.
CC PROSITE; PS00483; DIHYDROOROTASE_2; 1.
CC Pyrimidine biosynthesis; Hydrolyase; Zinc.
CC METAL 60 62 ZINC (POTENTIAL).
CC FT METAL 62 62 ZINC (POTENTIAL).
CC SQ SEQUENCE 427 AA; 46047 MW; 759A2AA99F733F4E CRC64;

Query Match      39.1%; Score 43; DB 1; Length 427;
Best Local Similarity 68.8%; Pred. No. 15;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TGVEGLKQDWDGATIK 19
DB 342 TGVEFLKQDVLDTIK 357

RESULT 11
ALAL_CANFA
ID ALAL_CANFA STANDARD; PRT; 1021 AA
AC P50997;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sodium/potassium-transporting ATPase alpha-1 chain precursor
DE (EC 3.6.3.9). (Sodium pump 1) (Na+/K+ ATPase 1).
GN ATP1A1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;

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QY      9 LQQDWGATY 18
|      | | | | |
DDB     143 LQQDWGATL 152

RESULT 14
-----
DDBA_STRCO STANDARD; PRT; 656 AA;
DDBA_STRCO
P27902; Q9KXX4;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Chromosomal replication initiator protein dnaA.
DnaA ORF SCH18.16C.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
[1]
SEQUENCE FROM N.A.
RP STRAIN=A3(2);
MEDLINE=92250416; PubMed=1577691;
Calcutt M.J., Schmidt F.J.;
"Conserved gene arrangement in the origin region of the Streptomyces
coelicolor chromosome."
J. Bacteriol. 174:3220-3226(1992).
[2]
SEQUENCE OF 51-656 FROM N.A.
RP STRAIN=A3(2);
Brown S.P., Harris D., Cerdeno A.M., Parkhill J., Barrell B.G.,
Rajandream M.A.;
Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
1. FUNCTION: PLAYS AN IMPORTANT ROLE IN THE INITIATION AND REGULATION
OF CHROMOSOMAL REPLICATION. BINDS TO THE ORIGIN OF REPLICATION;
IT BINDS SPECIFICALLY DOUBLE-STRANDED DNA AT A 9 BP CONSENSUS
(DNAA BOX): 5'-TTATC(C/A)A(C/A)A-3'. DNAA BINDS TO ATP AND TO
ACIDIC PHOSPHOLIPIDS.
1. SIMILARITY: BELONGS TO THE DNAA FAMILY.
-----
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EMBL; AF187159; AAA26734.1;
EMBL; AL357152; CAB92999.1;
PIR; A41870; A41870...
InterPro; IPR003593; AAA.
InterPro; IPR001957; Bac_DnaA.
Pfam; PF00308; bac_dnaA; 1.
PRINTS; PR00051; DNAA.
SMART; SM00382; AAA; 1.
PROSITE; PS01008; DNAA; 1.
DNA replication; DNA-binding; ATP-binding.
NP_BIND 357 364
SEQUENCE 656 AA; 73182 MW; 6CID5C0193D3C92B CRC64;

Query Match 38.2%; Score 42; DB 1; Length 656;
Best Local Similarity 36.8%; Pred. No. 35;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY      2 TTGTVFLKQDWGATIKD 20
|      | | | | |

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RESULT	15
A1A2_	HUMAN
ID	A1A2 HUMAN
STANDARD:	
PRT:	1020 AA.

PS0993; Q07059;
 01-OCT-1996 (Rel. 34, Created)
 01-OCT-1996 (Rel. 34, Last-annotation-update)
 15-OCT-2001 (Rel. 40, Last-annotation-update)
 Sodium/potassium-transporting ATPase alpha-2 chain precursor
 (EC 3.6.3.9) (Sodium pump 2) (Na+/K+ ATPase 2).
 ATP1A2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90008924; PubMed=2477373;
 RX Shull M.M., Pugh D.G., Lingrel J.B.;
 RT "Characterization of the human Na,K-ATPase alpha 2 gene and
 RT identification of intragenic restriction fragment length
 RT polymorphisms."
 RL J. Biol. Chem. 264:17532-17543(1989).
 RN [2]
 RP SEQUENCE OF 211-249 FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE=87231946; PubMed=3035563;
 RA Shull M.M., Lingrel J.B.;
 RT "Multiple genes encode the human Na+,K+-ATPase catalytic subunit."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4039-4043(1987).
 RN [3]
 RP SEQUENCE OF 251-442 FROM N.A.
 RC TISSUE=Placenta, and Brain;
 RX MEDLINE=87247232; PubMed=3036582;
 RA Sverdlov E.D., Monastyrskaya G.S., Broude N.E., Ushkaryov Y.A.,
 RA Allikmets R.L., Melkov A.M., Smirnov Y.V., Malyshov I.V.,
 RA Kostova I.E., Petrukhin K.E., Grishin A.V., Kijatkin N.I.,
 RA Kustova M.B., Sverdlov V.E., Modyanov N.N., Ovchinnikov Y.A.;
 RT "The family of human Na+,K+-ATPase genes: No less than five genes
 RT and/or pseudogenes related to the alpha-subunit."
 RL FEBS Lett. 217:275-278(1987).
 RN [4]
 RP SEQUENCE OF 1-4 FROM N.A.
 RX MEDLINE=89153603; PubMed=2537767;
 RA Sverdlov E.D., Bessarab D.A., Malyshov I.V., Petrukhin K.E.,
 RA Smirnov Y.V., Ushkaryov Y.A., Monastyrskaya G.S., Broude N.E.,
 RA Modyanov N.N.;
 RT "Family of human Na+,K+-ATPase genes. Structure of the putative
 RT regulatory region of the alpha+-gene."
 RL FEBS Lett. 244:481-483(1989).
 CC -1- FUNCTION: THIS IS THE CATALYTIC COMPONENT OF THE ACTIVE ENZYME,
 CC NA AND K IONS ACROSS THE PLASMA MEMBRANE. THIS ACTION CREATES THE
 CC ELECTROCHEMICAL GRADIENT OF NA AND K, PROVIDING THE ENERGY FOR
 CC ACTIVE TRANSPORT OF VARIOUS NUTRIENTS.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + Na(+)(In) + K(+)(Out) = ADP +
 CC phosphate + Na(+)(Out) + K(+)(In).
 CC -1- SUBUNIT: COMPOSED OF THREE SUBUNITS: ALPHA (CATALYTIC), BETA
 CC AND GAMMA.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
 CC (E1-E2 ATPASES). SUBFAMILY IIC.
 CC -----
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 CC -----
 CC EMBL; J05096; AAA51797.1;
 CC EMBL; M16795; AAA51799.1;
 CC EMBL; M27578; AAA35575.1;
 CC EMBL; M27571; AAA35575.1; JOINED.
 CC EMBL; M27576; AAA35575.1; JOINED.
 CC EMBL; Y07494; CAA68793.1; ALT_SEQ.

DR HSP; P04191; LEUL.
 DR MIM; 182340;
 DR InterPro; IPR004014; Cation_ATPase.
 DR InterPro; IPR001757; E1-E2_ATPase.
 DR InterPro; IPR001454; Hydrolase.
 DR InterPro; IPR000661; Na_K_ATPase.
 DR Pfam; PF00889; Cation_ATPase_C; 1.
 DR Pfam; PF00690; Cation_ATPase_N; 1.
 DR Pfam; PF00702; E1-E2_ATPase; 1.
 DR Pfam; PF00702; Hydrolase; 1.
 DR PRINTS; PR00119; CATATPASE.
 DR PRINTS; PR00121; NAKATPASE.
 DR PROSITE; PS00154; ATPASE_E1_E2; 1.
 DR Hydroxylase; Sodium/potassium transport; Transmembrane; Phosphorylation;
 KW Magnesium; Metal-binding; ATP-binding; Multigene family.
 FT PROPEP 1 5
 FT CHAIN 6 1020
 FT DOMAIN 6 85
 FT TRANSMEM 86 106
 FT DOMAIN 107 129
 FT TRANSMEM 130 150
 FT DOMAIN 151 286
 FT TRANSMEM 287 306
 FT DOMAIN 307 318
 FT TRANSMEM 319 336
 FT DOMAIN 337 769
 FT TRANSMEM 770 789
 FT DOMAIN 790 799
 FT TRANSMEM 800 820
 FT DOMAIN 821 840
 FT TRANSMEM 841 863
 FT DOMAIN 864 935
 FT TRANSMEM 936 948
 FT DOMAIN 949 967
 FT TRANSMEM 968 982
 FT DOMAIN 983 1003
 FT TRANSMEM 1004 1020
 FT MOD_RES 374 374
 FT MOD_RES 940 940
 FT BINDING 80 82
 FT METAL 714 714
 FT METAL 718 718
 FT SEQUENCE 1020 AA; 112265 MW; AFBDBEA94FFB4FC3 CRC64;
 SQ
 Query Match 38.2%; Score 42; DB 1; Length 1020;
 Best Local Similarity 40.0%; Pred. No. 57;
 Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 6 VFGLKQDWDGATIKD 20
 Db 880 LIGRLDWDPTDND 894

Search completed: June 7, 2002, 14:33:58
 Job time: 200 sec

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OM protein - protein search, using sw model

Run on: June 7, 2002, 14:30:18 ; Search time 25.04 seconds
(without alignments)
138.175 Million cell updates/sec

Title: US-10-054-647-2

Perfect score: 110

Sequence: 1 NTTCVFLKQWDGATIKD 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum: DB seq length: 0

Maximum: DB seq length: 2000000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 summaries

Database: 1: SPREMBL19:*

2: sp_archaea:*

3: sp_bacteria:*

4: sp_fungi:*

5: sp_human:*

6: sp_invertebrate:*

7: sp_mammal:*

8: sp_mhc:*

9: sp_organelle:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	pb	ID	Description
1	110	100.0	286	2	Q9ZGJ2	Q9ZGJ2 ehrlichia c
2	96	87.3	280	2	O52107	O52107 ehrlichia c
3	90	81.8	280	2	O85357	O85357 ehrlichia c
4	86	78.2	246	2	Q9RH35	Q9RH35 ehrlichia c
5	86	78.2	275	2	Q93DD4	Q93DD4 ehrlichia c
6	86	78.2	276	2	O85817	O85817 ehrlichia c
7	86	78.2	276	2	Q93DD1	Q93DD1 ehrlichia c
8	82	74.5	276	2	O85358	O85358 ehrlichia c
9	82	74.5	281	2	Q9AC19	Q9AC19 ehrlichia c
10	82	74.5	281	2	Q93DD2	Q93DD2 ehrlichia c
11	81	73.6	280	2	Q9ZGM9	Q9ZGM9 ehrlichia c
12	81	73.6	280	2	O85816	O85816 ehrlichia c
13	81	73.6	280	2	Q93DD3	Q93DD3 ehrlichia c
14	77	70.0	280	2	Q9ADV3	Q9ADV3 ehrlichia c
15	77	70.0	280	2	Q9F473	Q9F473 ehrlichia c
16	76	69.1	276	2	Q9F475	Q9F475 ehrlichia c

17	71	64.5	286	2	O52105	O52105 ehrlichia c
18	70	63.6	278	2	Q9F472	Q9F472 ehrlichia c
19	70	63.6	278	2	Q9R8A9	Q9R8A9 ehrlichia c
20	70	63.6	278	2	Q9R8A8	Q9R8A8 ehrlichia c
21	70	63.6	278	2	Q9R8A7	Q9R8A7 ehrlichia c
22	70	63.6	278	2	Q9R8A6	Q9R8A6 ehrlichia c
23	70	63.6	278	2	Q9R8A5	Q9R8A5 ehrlichia c
24	70	63.6	278	2	Q9R3J3	Q9R3J3 ehrlichia c
25	70	63.6	307	2	Q9ZGJ1	Q9ZGJ1 ehrlichia c
26	61.5	55.9	270	2	Q9AF98	Q9AF98 cowdria rum
27	61.5	55.9	277	2	Q93E57	Q93E57 cowdria rum
28	61.5	55.9	278	2	Q93E56	Q93E56 cowdria rum
29	61.5	55.9	278	2	Q93E52	Q93E52 cowdria rum
30	61.5	55.9	290	2	Q46324	Q46324 cowdria rum
31	61.5	55.9	290	2	Q46332	Q46332 cowdria rum
32	61.5	55.9	290	2	Q93E54	Q93E54 cowdria rum
33	61.5	55.9	290	2	Q9AEU3	Q9AEU3 cowdria rum
34	60	54.5	290	2	Q9AF99	Q9AF99 cowdria rum
35	59.5	54.1	265	2	Q93E59	Q93E59 cowdria rum
36	59.5	54.1	275	2	Q93E60	Q93E60 cowdria rum
37	59.5	54.1	276	2	Q93E53	Q93E53 cowdria rum
38	59.5	54.1	276	2	Q9R425	Q9R425 cowdria rum
39	59.5	54.1	287	2	Q46329	Q46329 cowdria rum
40	59.5	54.1	287	2	Q46331	Q46331 cowdria rum
41	59.5	54.1	287	2	Q46333	Q46333 cowdria rum
42	59.5	54.1	290	2	Q46330	Q46330 cowdria rum
43	59.5	54.1	290	2	Q9AMF6	Q9AMF6 cowdria sp.
44	59	53.6	272	2	Q93E54	Q93E54 cowdria rum
45	59	53.6	272	2	Q93E54	Q93E54 cowdria rum

ALIGNMENTS

RESULT 1

Q9ZGJ2	Q9ZGJ2	PRELIMINARY;	PRT; 288 AA.
AC	Q9ZGJ2;		
DT	01-MAY-1999 (TREMBLrel. 10, Created)		
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)		
DE	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	30-KDA MAJOR OUTER MEMBRANE PROTEIN (P28-8).		
GN	P30 OR P28-8.		
OS	Ehrlichia canis.		
OC	Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;		
OC	Rickettsiaceae; Ehrlichieae; Ehrlichia.		
OX	NCBI_TaxID:944;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-OKLAHOMA;		
RX	MEDLINE-98371112; PubMed-9705412;		
RA	Ohashi N., Unver A., Zhi N., Rikihisa Y.;		
RT	"Cloning and characterization of multigenes encoding the		
RT	immunodominant 30-kilodalton major outer membrane proteins of		
RT	Ehrlichia canis and application of the recombinant protein for		
RT	serodiagnosis."		
RL	J. Clin. Microbiol. 36:2671-2680(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-JAKE;		
RX	MEDLINE-99242757; PubMed-10225842;		
RA	McBride J.W., Yu, Xj, Walker D.H.;		
RT	"Molecular cloning of the gene for a conserved major immunoreactive		
RT	28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic		
RT	antigen."		
RL	Clin. Diagn. Lab. Immunol. 6:392-399(1999).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-JAKE;		
RX	MEDLINE-20432107; PubMed-10974556;		
RA	McBride J.W., Yu X.J., Walker D.H.;		
RT	"A conserved, transcriptionally active p28 multigene locus of		
RT	Ehrlichia canis."		

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OC Rickettsiaceae; Ehrlichiae; Ehrlichia.
OX NCBI_TaxID=945;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-V2;
RA Long S.W., Zhang X.-F., Qi H., Standaert S., Walker D.H., Yu X.-J.;
RT "Allele variation and patterns of transcription of the Ehrlichia
chaffeensis 28 kDa outer membrane protein multigene family";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF393389; AAL12919.1;
SQ SEQUENCE 275 AA; 29974 MW; 2ECC2F988B2E9D9 CRC64;

Query Match 78.2%; Score 86; DB 2; Length 275;
Best Local Similarity 83.3%; Pred. No. 2.e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NTTGVFGLKQDWDGATI 18
||| |||||||||
DB 59 NTTAGVFLKQDWDGSAI 76

RESULT 6
ID O85817 PRELIMINARY; PRT; 276 AA.
AC O85817;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN P28.
OS Ehrlichia chaffeensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Ehrlichiae; Ehrlichia.
OX NCBI_TaxID=945;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-SAPULPA;
RX MEDLINE-99175287; PubMed=10074538;
RA Yu X.-J., McBride J.W., Walker D.H.;
RT "Genetic diversity of the 28-kilodalton outer membrane protein gene in
human isolates of Ehrlichia chaffeensis";
RL J. Clin. Microbiol. 37:1137-1143(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-SAPULPA;
RA Yu X.-J., Walker D.H.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN-V9;
RA Long S.W., Zhang X.-F., Qi H., Standaert S., Walker D.H., Yu X.-J.;
RT "Allele variation and patterns of transcription of the Ehrlichia
chaffeensis 28 kDa outer membrane protein multigene family";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF077734; AAC31547.1;
DR EMBL: AF393395; AAL12925.1;
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 1.
SQ SEQUENCE 276 AA; 30027 MW; 2FD3698FCF1F60BE CRC64;

Query Match 78.2%; Score 86; DB 2; Length 276;
Best Local Similarity 83.3%; Pred. No. 2.e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NTTGVFGLKQDWDGATI 18
||| |||||||||
DB 59 NTTAGVFLKQDWDGSAI 76

RESULT 7
ID Q93DD1 PRELIMINARY; PRT; 276 AA.

AC Q93DD1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN P28.
OS Ehrlichia chaffeensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Ehrlichiae; Ehrlichia.
OX NCBI_TaxID=945;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-V7;
RA Long S.W., Zhang X.-F., Qi H., Standaert S., Walker D.H., Yu X.-J.;
RT "Allele variation and patterns of transcription of the Ehrlichia
chaffeensis 28 kDa outer membrane protein multigene family";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF393393; AAL12923.1;
SQ SEQUENCE 276 AA; 30028 MW; 2D7143AFCBFF2EBE CRC64;

Query Match 78.2%; Score 86; DB 2; Length 276;
Best Local Similarity 83.3%; Pred. No. 2.e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NTTGVFGLKQDWDGATI 18
||| |||||||||
DB 59 NTTAGVFLKQDWDGSAI 76

RESULT 8
ID O85358 PRELIMINARY; PRT; 276 AA.
AC O85358;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 28 KDA MAJOR SURFACE ANTIGEN-5 (FRAGMENT)
OS Ehrlichia chaffeensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Ehrlichiae; Ehrlichia.
OX NCBI_TaxID=945;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-ARKANSAS;
RX MEDLINE-98321180; PubMed=9647746;
RA Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
RA Allen A.R.;
RT "Molecular characterization of a 28 kDa surface antigen gene family of
the tribe Ehrlichiae";
RL Biochem. Biophys. Res. Commun. 247:636-643(1998).
DR EMBL: AF062761; AAC26716.1;
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 1.
FT NON_TER 276
FT SEQUENCE 276 AA; 29782 MW; A9AB2A92263CA4EA CRC64;

Query Match 74.5%; Score 82; DB 2; Length 276;
Best Local Similarity 70.0%; Pred. No. 8.6e-05;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 NTTGVFGLKQDWDGATI 20
||| |||||||||
DB 59 NTTGVFGLKQDWDGSAIN 78

RESULT 9
ID Q9ACI9 PRELIMINARY; PRT; 281 AA.
AC Q9ACI9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE MAJOR OUTER MEMBRANE PROTEIN P28.
 OS Ehrlichia chaffeensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Ehrlichieae; Ehrlichia.
 OX NCBI_TaxID=945;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ARKANSAS;
 RX MEDLINE=98084465; PubMed=9423849;
 RA Ohashi N., Zhi N., Zhang Y., Rikihisa Y.
 RT "Immunodominant major outer membrane proteins of Ehrlichia chaffeensis
 are encoded by a polymorphic multigene family."
 RL Infect. Immun. 66:132-139(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ARKANSAS;
 RX MEDLINE=21153566; PubMed=11254561;
 RA Ohashi N., Rikihisa Y., Unver A.
 RT "Analysis of transcriptionally Active Gene Clusters of Major Outer
 Membrane Protein Multigene Family in Ehrlichia canis and E.
 chaffeensis."
 RL Infect. Immun. 69:2083-2091(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-V1;
 RA Long S.W., Zhang X.-F., Qi H., Standaert S., Walker D.H., Yu X.-J.;
 RT "Allele variation and patterns of transcription of the Ehrlichia
 chaffeensis 28 kDa outer membrane protein multigene family."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U72291; AAK28673.1;
 DR EMBL; AF393388; AAL12918.1;
 DR InterPro: IPR002566; Surface_Ag_msp4.
 DR Pfam: PF01617; Surface_Ag_2; 1.
 DR SEQUENCE 281 AA; 30343 MW; A995F7C4459AA9A CRC64;
 SQ

Query Match 74.5%; Score 82; DB 2; Length 281;
 Best Local Similarity 70.0%; Pred. No. 8.7e-05;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 NTTCVFGKQDWDGATIKD 20
 ||| |||||:||||:|
 Db 59 NTTGVFGLKQNDGSAISN 78

RESULT 10
 ID Q93DD2 PRELIMINARY; PRT; 281 AA.
 AC Q93DD2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE OUTER MEMBRANE PROTEIN P28.
 OS Ehrlichia chaffeensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Ehrlichieae; Ehrlichia.
 OX NCBI_TaxID=945;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-V6;
 RX Long S.W., Zhang X.-F., Qi H., Standaert S., Walker D.H., Yu X.-J.;
 RT "Allele variation and patterns of transcription of the Ehrlichia
 chaffeensis 28 kDa outer membrane protein multigene family."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF393392; AAL12922.1;
 DR SEQUENCE 281 AA; 30388 MW; B54DBB55AC839A9A CRC64;
 SQ

Query Match 74.5%; Score 82; DB 2; Length 281;
 Best Local Similarity 70.0%; Pred. No. 8.7e-05;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 NTTCVFGKQDWDGATIKD 20
 ||| |||||:||||:|
 Db 59 NTTGVFGLKQNDGSAISN 78

RESULT 11
 Q92GM9 PRELIMINARY; PRT; 280 AA.
 ID Q92GM9
 AC Q92GM9;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE OUTER MEMBRANE PROTEIN P28.
 OS Ehrlichia chaffeensis
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Ehrlichieae; Ehrlichia.
 OX NCBI_TaxID=945;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAX;
 RX MEDLINE=99175287; PubMed=10074538;
 RA Yu X.-J., McBride J.W., Walker D.H.;
 RT "Genetic diversity of the 28-kilodalton outer membrane protein gene in
 human isolates of Ehrlichia chaffeensis."
 RL J. Clin. Microbiol. 37:1137-1143(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAX;
 RA Yu X.-J., Walker D.H.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF077733; AAC31546.1;
 DR InterPro: IPR002566; Surface_Ag_msp4.
 DR Pfam: PF01617; Surface_Ag_2; 1.
 DR SEQUENCE 280 AA; 30304 MW; 91C5AC7851B77F2 CRC64;
 SQ

Query Match 73.6%; Score 81; DB 2; Length 280;
 Best Local Similarity 77.8%; Pred. No. 0.00012;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NTTCVFGKQDWDGATIKD 18
 ||| |||||:||||:|
 Db 59 STTAGVFGKQNDGSAI 76

RESULT 12
 ID O85816 PRELIMINARY; PRT; 280 AA.
 AC O85816;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE OUTER MEMBRANE PROTEIN P28.
 OS Ehrlichia chaffeensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Ehrlichieae; Ehrlichia.
 OX NCBI_TaxID=945;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-91HE17;
 RX Yu X.-J., McBride J.W., Walker D.H.;
 RT "Genetic diversity of the 28-kilodalton outer membrane protein gene in
 human isolates of Ehrlichia chaffeensis."
 RL J. Clin. Microbiol. 37:1137-1143(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-91HE17;
 RA Yu X.-J., Walker D.H.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-V8, AND V4;

RA Long S.W., Zhang X.-F., Qi H., Standaert S., Walker D.H., Yu X.-J.;
RT "Allele variation and patterns of transcription of the Ehrlichia
RT chaffeensis 28 kDa outer membrane protein multigene family";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF077732; AAC31545.1; -
DR EMBL: AF393394; AAL12924.1; -
DR EMBL: AF393390; AAL12920.1; -
DR InterPro: IPR002566; Surface_Ag_msp4.
DR Pfam: PF01617; Surface_Ag_2; 1.
SQ SEQUENCE 280 AA; 30277 MW; 91C54AC78507A63F CRC64;

Query Match 73.6%; Score 81; DB 2; Length 280;
Best Local Similarity 77.8%; Pred. No. 0.00012;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NTGTGVLGKQDWDGATI 18
DB 59 STTAGVFLGKQDWDGSAI 76

RESULT 13
ID Q93DD3 PRELIMINARY; PRT; 280 AA.
AC Q93DD3; 2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN P28.
OS Ehrlichia chaffeensis
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Ehrlichieae; Ehrlichia.
OX NCBI_TaxID=945;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-V5;
RA Long S.W., Zhang X.-F., Qi H., Standaert S., Walker D.H., Yu X.-J.;
RT "Allele variation and patterns of transcription of the Ehrlichia
RT chaffeensis 28 kDa outer membrane protein multigene family";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF393391; AAL12921.1; -
SQ SEQUENCE 280 AA; 30372 MW; C7B8C8710BC167E9 CRC64;

Query Match 73.6%; Score 81; DB 2; Length 280;
Best Local Similarity 77.8%; Pred. No. 0.00012;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NTGTGVLGKQDWDGATI 18
DB 59 STTAGVFLGKQDWDGSAI 76

RESULT 14
ID Q9ADV3 PRELIMINARY; PRT; 280 AA.
AC Q9ADV3; 2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE MAJOR OUTER MEMBRANE PROTEIN P30-2.
GN P30-2.
OS Ehrlichia canis.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Ehrlichieae; Ehrlichia.
OX NCBI_TaxID=944;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OKLAHOMA;
RX MEDLINE=98371112; PubMed=9705412;
RA Ohashi N., Unver A., Zhi N., Rikihisa Y.;
RT "Cloning and characterization of multigenes encoding the
RT immunodominant 30-kilodalton major outer membrane proteins of

RT Ehrlichia canis and application of the recombinant protein for
RT serodiagnosis";
RL J. Clin. Microbiol. 36:2671-2680(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-OKLAHOMA;
RX MEDLINE=21153586; PubMed=11254561;
RA Ohashi N., Rikihisa Y., Unver A.;
RT "Analysis of Transcriptionally Active Gene Clusters of Major Outer
RT Membrane Protein Multigene Family in Ehrlichia canis and E.
RT chaffeensis";
RL Infect. Immun. 69:2083-2091(2001).
DR EMBL: AF078553; AAK28699.1; -
DR InterPro: IPR002566; Surface_Ag_msp4.
DR Pfam: PF01617; Surface_Ag_2; 1.
SQ SEQUENCE 280 AA; 30803 MW; 27238BE1C7E68A91 CRC64;

Query Match 70.0%; Score 77; DB 2; Length 280;
Best Local Similarity 65.0%; Pred. No. 0.00052;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 NTGTGVLGKQDWDGATI 20
DB 59 NSTGVFLGKHDWNGGTISN 78

RESULT 15
ID Q9F473 PRELIMINARY; PRT; 280 AA.
AC Q9F473; 2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE P28-6.
GN P28-6.
OS Ehrlichia canis.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Ehrlichieae; Ehrlichia.
OX NCBI_TaxID=944;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAKE;
RX MEDLINE=99242757; PubMed=10225842;
RA McBride J.W., Yu X.J., Walker D.H.;
RT "Molecular cloning of the gene for a conserved major immunoreactive
RT 28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic
RT antigen";
RL Clin. Diagn. Lab. Immunol. 6:392-399(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-JAKE;
RX MEDLINE=20432107; PubMed=10974556;
RA McBride J.W., Yu X.J., Walker D.H.;
RT "A conserved, transcriptionally active p28 multigene locus of
RT Ehrlichia canis";
RL Gene 254:245-252(2000).
DR EMBL: AF082744; AAG14361.1; -
DR InterPro: IPR002566; Surface_Ag_msp4.
DR Pfam: PF01617; Surface_Ag_2; 1.
SQ SEQUENCE 280 AA; 30762 MW; BE284A4B94FE3123 CRC64;

Query Match 70.0%; Score 77; DB 2; Length 280;
Best Local Similarity 65.0%; Pred. No. 0.00052;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 NTGTGVLGKQDWDGATI 20
DB 59 NSTGVFLGKHDWNGGTISN 78

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Job time: 203 sec

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